Innovation in Metabolomics: A New Standard Reference Material for Metabolites in Human Plasma

NIST is working with NIH to develop a human blood plasma-based Standard Reference Material (SRM) containing up to 100 biomolecules of known concentrations. SRM 1950 will enable evaluation of new procedures and equipment for measuring metabolites and improve the reproducibility of measurements by providing a stable standard for comparison. These measurements may provide insight into the chemical and molecular pathways that are involved in normal function as well as disease. The National Institutes of Health (NIH) Metabolomics Technology Development Initiative reflects the need for new tools to identify and quantify metabolites in human systems.

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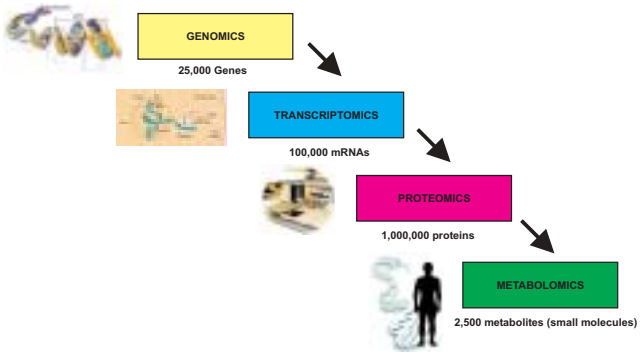
NIST is developing a plasma-based Standard Reference Material (SRM) to support technology development in the field of metabolomics. Metabolomics is a relatively new field that builds upon ongoing work in genomics and proteomics. The goal of metabolomics is to identify, measure, and interpret the complex profile of metabolites in cells, tissues, and other biological samples. The metabolome represents the collection of all metabolites in an organism at a particular moment in time. Because metabolites constitute the end products of gene expression, metabolomics may provide a unique mechanism to examine genotype-phenotype relationships. Metabolomics is increasingly being used in health-related applications, including drug development, and may ultimately lead to better disease diagnosis and treatment.

NIST's new SRM 1950 Metabolites in Human Plasma was developed in response to requests from the scientific community for a resource that would enable better inter-laboratory comparisons of measurements of critical metabolites.

Metabolomics has been identified in the NIH Roadmap for Medical Research as an important tool in understanding cellular pathways in normal and disease states. The complexity of the metabolome poses significant analytical challenges because hundreds of metabolites may be detected in a single sample. Analytical techniques that are currently used for metabolomics research include chromatography, mass spectrometry, and nuclear magnetic resonance (NMR) spectroscopy. At the present time, however, the human metabolome remains poorly characterized, and normal levels have only been established for a limited number of metabolites. As a result, interpretation of the physiological significance of metabolite concentrations remains difficult, and most investigations have been qualitative, rather than quantitative in nature.



The NIH Roadmap Metabolomics Technology Development Initiative is intended to promote the discovery of novel technologies to enhance understanding of metabolic pathways and networks. Discussions among roadmap investigators and between NIH and NIST identified a need for a reference material to support metabolomics technology development. The new SRM 1950 Metabolites in Human Plasma will assist the metabolomics community by providing a material with well-characterized concentrations of up to 100 metabolites at normal physiological levels and was designed in consultation with NIH and the roadmap investigators. The SRM is designed to serve as a tool to benchmark the development of new technology and will facilitate the move toward quantitative technologies for examining changing metabolite concentrations.

NIH Roadmap FOR MEDICAL RESEARCH

Development of SRM 1950, NIST's first plasma-based SRM, is underway. The SRM will consist of a plasma pool collected from an equal number of men and women and with a racial distribution that reflects the U.S. population. The initial value assignment phase for this SRM will include approximately 50 metabolites for which NIST has existing methods (e.g., cholesterol, electrolytes, glucose, hormones). Additional information for value assignment will be provided by collaborating laboratories to which the candidate SRM is distributed. NIST will develop methods for additional high-priority analytes, as identified by NIH, during the second phase of value assignment.